



SEQUENCE LISTING

RECEIVED
FEB 15 2002
TECH CENTER 1600/2900

<110> Immusol Incorporated
Welch, Peter J.
Barber, Jack R.

<120> Tumor Suppressor Molecules and Methods
of Use

<130> 039316-0301

<140> US 09/438,917

<141> 1999-11-12

<160> 20

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 16

<212> RNA

<213> Artificial Sequence

<220>

<223> hairpin ribozyme

<400> 1

accuccccag aacccu

16

<210> 2

<211> 16

<212> RNA

<213> homo sapiens

<220>

<221> misc_feature

<222> (1)...(16)

<223> n = A,U,C or G

<400> 2

aggngucgg ggaggu

16

<210> 3
<211> 16
<212> RNA
<213> Artificial Sequence

<220>

<223> hairpin ribozyme

<400> 3

agaguguaag aaacua

16

<210> 4
<211> 16
<212> RNA
<213> homo sapiens

<220>

<221> misc_feature

<222> (1)...(16)

<223> n = A,U,C or G

<400> 4

uagungucua cacucu

16

AI
cont
<210> 5
<211> 1664
<212> DNA
<213> homo sapiens

<220>

<221> CDS

<222> (103)...(1525)

<400> 5

gcctgatgtc gtcccacgccc gtgcggctc tcaggcgccg gaagttagct ggcacggcc 60
gaaagcgccg gacgcaggag gcctcggtgg a gacacagca gc atg gga cag tca 114
Met Gly Gln Ser
m 6 a s

ggg agg tcc cgg cac cag aag cgc gcc ccg ccc cag gcg cag ctc cgc 162
Gly Arg Ser Arg His Gln Lys Arg Ala Pro Pro Gln Ala Gln Leu Arg

5 G R S R H 10 Q K R A P P 15 Q A Q L R 20

aac ctc gag gcc tat gcc gcg aac ccg cac tcg ttc gtg ttc acg cga 210
Asn Leu Glu Ala Tyr Ala Ala Asn Pro His Ser Phe Val Phe Thr Arg

N L E A 25 Y A A N P 30 H S F V F T 35 R

ggc tgc acg ggt cgc aac atc cgg cag ctc agc ctg gac gtg cgg cgg 258
 Gly Cys Thr Gly Arg Asn Ile Arg Gln Leu Ser Leu Asp Val Arg Arg
 6 C T ⁴⁰ G R N I R Q ⁴⁵ L S L D ⁵⁰ V R R
 gtc atg gag ccc gtc act gcc agc cgt ctg cag gtt cgt aag aag aac 306
 Val Met Glu Pro Val Thr Ala Ser Arg Leu Gln Val Arg Lys Lys Asn
 V M ⁵⁵ E P V T A ⁶⁰ S R L Q V R L L N
 tcg ctg aag gac tgc gtc gca gtc gct ggg ccc ctc ggg gtc aca cac 354
 Ser Leu Lys Asp Cys Val Ala Val Ala Gly Pro Leu Gly Val Thr His
 S L ⁷⁰ K D C V A ⁷⁵ V A G P ⁸⁰ L G V T H
 ttt ctg atc cta gca aaa caa gag acc aat gtc tac ttt aag ctg atg 402
 Phe Leu Ile Leu Ala Lys Gln Glu Thr Asn Val Tyr Phe Lys Leu Met
 F L ⁸⁵ I L A K Q E T N ⁹⁰ V Y F K L ¹⁰⁰ M
 cgc ctc cca gga ggc ccc acc ttg acc ttc cag gtc aag aag tac tcg 450
 Arg Leu Pro Gly Gly Pro Thr Leu Thr Phe Gln Val Lys Lys Tyr Ser
 R L P F ¹⁰⁵ P T V T P Q V K K ¹¹⁰ Y ¹¹⁵ S
 ctg gtg cgt gat gtg gtc tcc tca ctg cgc cgg cac cgc atg cac gag 498
 Leu Val Arg Asp Val Val Ser Ser Leu Arg Arg His Arg Met His Glu
 L V R ¹²⁰ V V S S ¹²⁵ E R R H R ¹³⁰ M H E
 cag cag ttt gcc cac cca ccc ctc ctg gta ctc aac agc ttt ggc ccc 546
 Gln Gln Phe Ala His Pro Pro Leu Leu Val Leu Asn Ser Phe Gly Pro
 Q Q F A H P P ¹³⁵ L V L N ¹⁴⁰ S ¹⁴⁵ F G P
 cat ggt atg cat gtg aag ctc atg gcc acc atg ttc cag aac ctg ttc 594
 His Gly Met His Val Lys Leu Met Ala Thr Met Phe Gln Asn Leu Phe
 H ¹⁵⁰ M H V K L M A T M F Q D L F
 ccc tcc atc aac gtg cac aag gtg aac ctg aac acc atc aag cgc tgc 642
 Pro Ser Ile Asn Val His Lys Val Asn Leu Asn Thr Ile Lys Arg Cys
 P S I N V ¹⁶⁵ H K V N L ¹⁷⁰ N T I K R ¹⁷⁵ C ¹⁸⁰ C
 ctc ctc atc gac tac aac ccc gac tcc cag gag ctg gac ttc cgc cac 690
 Leu Leu Ile Asp Tyr Asn Pro Asp Ser Gln Glu Leu Asp Phe Arg His
 L I D ¹⁸⁵ N P D S ¹⁹⁰ E L D F ¹⁹⁵ R H
 tat agc atc aaa gtt gtt cct gtg ggc gcg agt cgc ggg atg aag aag 738
 Tyr Ser Ile Lys Val Val Pro Val Gly Ala Ser Arg Gly Met Lys Lys
 Y S I K ²⁰⁰ V V P V ²⁰⁵ G A S R F ²¹⁰ M K K
 ctg ctc cag gag aag ttc ccc aac atg agc cgc ctg cag gac atc agc 786
 Leu Leu Gln Glu Lys Phe Pro Asn Met Ser Arg Leu Gln Asp Ile Ser
 L L Q L F P ²¹⁵ N M S R L ²²⁰ Q D I S
 gag ctg ctg gcc acg ggc gcg ggg ctg tcg gag agc gag gca gag cct 834
 Glu Leu Leu Ala Thr Gly Ala Gly Leu Ser Glu Ser Glu Ala Glu Pro
 Q ²³⁰ L A T S ²³⁵ G L S E S ²⁴⁰ Q A F P

gac ggc gac cac aac atc aca gag ctg cct cag gct gtc gct ggc cgt 882
 Asp Gly Asp His Asn Ile Thr Glu Leu Pro Gln Ala Val Ala Gly Arg
 245 G H 250 L P 255 A V A 260 R
 ggc aac atg cgg gcc cag cag agt gca gtg cgg ctc acc gag atc ggc 930
 Gly Asn Met Arg Ala Gln Gln Ser Ala Val Arg Leu Thr Glu Ile Gly
 G N M 265 S A 270 L 275
 ccg cgg atg aca ctg cag ctc atc aag gtc cag gag ggc gtc ggg gag 978
 Pro Arg Met Thr Leu Gln Leu Ile Lys Val Gln Glu Gly Val Gly Glu
 P R M 280 285 V 290 V
 ggc aaa gtg atg ttc cac agt ttt gtg agc aag acg gag gag gag ctg 1026
 Gly Lys Val Met Phe His Ser Phe Val Ser Lys Thr Glu Glu Glu Leu
 G 295 M F S 300 V L 305
 cag gcc atc ctg gaa gcc aag gag aag aag ctg cgg ctg aag gct cag 1074
 Gln Ala Ile Leu Glu Ala Lys Glu Lys Lys Leu Arg Leu Lys Ala Gln
 310 L A 315 L L 320
 A
 agg cag gcc cag cag gcc cag aat gtg cag cgc aag cag gag cag cgg 1122
 Arg Gln Ala Gln Ala Gln Asn Val Gln Arg Lys Gln Glu Gln Arg
 325 R A 330 N V 335 L 340
 gag gcc cac aga aag aag agc ctg gag ggc atg aag aag gca cgg gtc 1170
 Glu Ala His Arg Lys Lys Ser Leu Glu Gly Met Lys Lys Ala Arg Val
 A P R K S L D 345 350 M K K A 355
 ggg ggt agt gat gaa gag gcc tct ggg atc cct tca agg acg gcg agc 1218
 Gly Gly Ser Asp Glu Glu Ala Ser Gly Ile Pro Ser Arg Thr Ala Ser
 S 360 E E A S 365 P S R 370 A
 ctg gag ttg ggt gag gac gat gat gaa cag gaa gat gat gac atc gag 1266
 Leu Glu Leu Gly Glu Asp Asp His Glu Gln Glu Asp Asp Asp Ile Glu
 L 375 E 380 H 385 I
 tat ttc tgc cag gcg gtg ggc gag gcg ccc agt gag gac ctg ttc ccc 1314
 Tyr Phe Cys Gln Ala Val Gly Glu Ala Pro Ser Glu Asp Leu Phe Pro
 390 A V 395 E A P S 400 L F P
 gag gcc aag cag aaa cgg ctt gcc aag tct cca ggg cgg aag cgg aag 1362
 Glu Ala Lys Gln Lys Arg Leu Ala Lys Ser Pro Gly Arg Lys Arg Lys
 405 A L L 410 L A L S P 415 R R 420 L
 cgg tgg gaa atg gat cga ggc agg ggt cgc ctt tgt gac cag aag ttt 1410
 Arg Trp Glu Met Asp Arg Gly Arg Gly Arg Leu Cys Asp Gln Lys Phe
 R M 425 R S R G R 430 L C 435
 ccc aag acc aag gac aag tcc cag gga gcc cag gcc agg cgg ggg ccc 1458
 Pro Lys Thr Lys Asp Lys Ser Gln Gly Ala Gln Ala Arg Arg Gly Pro
 P 440 445 A A R R 450

aga ggg gct tcc cg^g gat ggt ggg cga ggc cg^g ggc cga ggc cgc cca 1506
Arg Gly Ala Ser Arg Asp Gly Gly Arg Gly Arg Gly Arg Gly Arg Pro
455 460 465

ggg aag aga gtg gcc tga g cccaa^gccgc accggagcag cggctggatt 1555
Gly Lys Arg Val Ala *
470

gaacgccccca gattggggcc cgagatgtgg ccctcggtt ccttcataaa aggagttgtg 1615
tccccagccc ttccactcca gtaaagaact gaattggcaa aaaaaaaaaa 1664

<210> 6
<211> 473
<212> PRT
<213> homo sapiens

<400> 6
Met Gly Gln Ser Gly Arg Ser Arg His Gln Lys Arg Ala Pro Pro Gln
1 5 10 15
Ala Gln Leu Arg Asn Leu Glu Ala Tyr Ala Ala Asn Pro His Ser Phe
20 25 30
Val Phe Thr Arg Gly Cys Thr Gly Arg Asn Ile Arg Gln Leu Ser Leu
35 40 45
Asp Val Arg Arg Val Met Glu Pro Val Thr Ala Ser Arg Leu Gln Val
50 55 60
Arg Lys Lys Asn Ser Leu Lys Asp Cys Val Ala Val Ala Gly Pro Leu
65 70 75 80
Gly Val Thr His Phe Leu Ile Leu Ala Lys Gln Glu Thr Asn Val Tyr
85 90 95
Phe Lys Leu Met Arg Leu Pro Gly Gly Pro Thr Leu Thr Phe Gln Val
100 105 110
Lys Lys Tyr Ser Leu Val Arg Asp Val Val Ser Ser Leu Arg Arg His
115 120 125
Arg Met His Glu Gln Gln Phe Ala His Pro Pro Leu Leu Val Leu Asn
130 135 140
Ser Phe Gly Pro His Gly Met His Val Lys Leu Met Ala Thr Met Phe
145 150 155 160
Gln Asn Leu Phe Pro Ser Ile Asn Val His Lys Val Asn Leu Asn Thr
165 170 175
Ile Lys Arg Cys Leu Leu Ile Asp Tyr Asn Pro Asp Ser Gln Glu Leu
180 185 190
Asp Phe Arg His Tyr Ser Ile Lys Val Val Pro Val Gly Ala Ser Arg
195 200 205
Gly Met Lys Lys Leu Leu Gln Glu Lys Phe Pro Asn Met Ser Arg Leu
210 215 220
Gln Asp Ile Ser Glu Leu Leu Ala Thr Gly Ala Gly Leu Ser Glu Ser
225 230 235 240
Glu Ala Glu Pro Asp Gly Asp His Asn Ile Thr Glu Leu Pro Gln Ala
245 250 255

Val Ala Gly Arg Gly Asn Met Arg Ala Gln Gln Ser Ala Val Arg Leu
260 265 270
Thr Glu Ile Gly Pro Arg Met Thr Leu Gln Leu Ile Lys Val Gln Glu
275 280 285
Gly Val Gly Glu Gly Lys Val Met Phe His Ser Phe Val Ser Lys Thr
290 295 300
Glu Glu Glu Leu Gln Ala Ile Leu Glu Ala Lys Glu Lys Lys Leu Arg
305 310 315 320
Leu Lys Ala Gln Arg Gln Ala Gln Gln Ala Gln Asn Val Gln Arg Lys
325 330 335
Gln Glu Gln Arg Glu Ala His Arg Lys Lys Ser Leu Glu Gly Met Lys
340 345 350
Lys Ala Arg Val Gly Gly Ser Asp Glu Glu Ala Ser Gly Ile Pro Ser
355 360 365
Arg Thr Ala Ser Leu Glu Leu Gly Glu Asp Asp Asp Glu Gln Glu Asp
370 375 380
Asp Asp Ile Glu Tyr Phe Cys Gln Ala Val Gly Glu Ala Pro Ser Glu
385 390 395 400
Asp Leu Phe Pro Glu Ala Lys Gln Lys Arg Leu Ala Lys Ser Pro Gly
405 410 415
Arg Lys Arg Lys Arg Trp Glu Met Asp Arg Gly Arg Gly Arg Leu Cys
420 425 430
Asp Gln Lys Phe Pro Lys Thr Lys Asp Lys Ser Gln Gly Ala Gln Ala
435 440 445
Arg Arg Gly Pro Arg Gly Ala Ser Arg Asp Gly Gly Arg Gly Arg Gly
450 455 460
Arg Gly Arg Pro Gly Lys Arg Val Ala
465 470

A
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<210> 7
<211> 87
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotides

<221> misc_feature
<222> (1)...(87)
<223> n = A,T,C or G

<400> 7
cgcgtaccag gtaatatacc acggaccgaa gtccgtgtgt ttctctggtn nnnttctnnn 60
nnnnnggatc ctgtttccgc ccggttt 87

<210> 8
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 8
gtccgtggta tattacctgg ta

22

<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 9
cgaaaccggg cgaaaaacagg

20

*Al
mt*
<210> 10
<211> 52
<212> RNA
<213> Artificial Sequence

<220>
<223> hairpin ribozyme

<221> misc_feature
<222> (1)...(52)
<223> n = A,U,C or G

<400> 10
nnnnnnnnnag aannnnacca gagaaacaca cguuguggua uauuaccugg ua

52

<210> 11
<211> 27
<212> DNA
<213> homo sapiens

<400> 11
ccatcctaat acgactcact atagggc

27

<210> 12
<211> 43
<212> DNA
<213> homo sapiens

<220>
<221> misc_feature
<222> (1)...(42)
<223> n = A,T,C or G

<400> 12
cgatgctcct ctagactcga gggtaaccacc tcccccacnc cct

43

<210> 13
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 13
ggccacgcgt cgactagtagtac tttttttttt tttttttv

38

W
W
<210> 14
<211> 20
<212> DNA
<213> homo sapiens

<400> 14
cggtcacccg agatcgcccc

20

<210> 15
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 15
ggccacgcgt cgactagtagtac t

21

<210> 16
<211> 429
<212> PRT
<213> mus musculus

<400> 16

Met Gly Gln Ser Gly Arg Ser Arg His Gln Lys Arg Asn Arg Ala Gln
1 5 10 15
Ala Gln Leu Arg Asn Leu Glu Ser Tyr Ala Ala Gln Pro His Ser Phe
20 25 30
Val Phe Thr Arg Gly Arg Ala Gly Arg Asn Val Arg Gln Leu Ser Leu
35 40 45
Asp Val Arg Arg Val Met Glu Pro Leu Thr Ala Thr Arg Leu Gln Val
50 55 60
Arg Lys Lys Asn Ser Leu Lys Asp Cys Val Ala Val Ala Gly Pro Leu
65 70 75 80
Gly Val Thr His Phe Leu Ile Leu Thr Lys Thr Cys Asn Ser Val Tyr
85 90 95
Leu Lys Leu Met Arg Leu Pro Gly Gly Pro Thr Leu Thr Phe Gln Ile
100 105 110
Ser Lys Tyr Thr Leu Ile Arg Asp Val Val Ser Ser Leu Arg Arg His
115 120 125
Arg Met His Glu Gln Gln Phe Asn His Pro Pro Leu Leu Val Leu Asn
130 135 140
Ser Phe Gly Pro Gln Ala Met His Ile Lys Leu Met Ala Thr Met Phe
145 150 155 160
Gln Asn Leu Phe Pro Ser Ile Asn Val His Thr Val Asn Leu Asn Thr
165 170 175
Ile Lys Arg Cys Leu Leu Ile Asn Tyr Asn Pro Asp Ser Gln Glu Leu
180 185 190
Asp Phe Arg His Tyr Ser Val Lys Val Val Pro Val Gly Ala Ser Arg
195 200 205
Gly Met Lys Lys Leu Leu Gln Glu Lys Phe Pro Asn Met Ser Arg Leu
210 215 220
Gln Asp Ile Ser Glu Leu Leu Ala Thr Gly Val Gly Leu Ser Asp Ser
225 230 235 240
Glu Val Glu Pro Asp Gly Glu His Asn Thr Thr Glu Leu Pro Gln Ala
245 250 255
Val Ala Gly Arg Gly Asn Met Gln Ala Gln Gln Ser Ala Val Arg Leu
260 265 270
Thr Glu Ile Gly Pro Arg Met Thr Leu Gln Leu Ile Lys Ile Gln Glu
275 280 285
Gly Val Gly Asn Gly Asn Val Leu Phe His Ser Phe Val His Lys Thr
290 295 300
Glu Glu Glu Leu Gln Ala Ile Leu Ala Ala Lys Glu Glu Lys Leu Arg
305 310 315 320
Leu Lys Ala Gln Arg Gln Asn Gln Gln Ala Glu Asn Leu Gln Phe Ser
325 330 335
Arg Ser Cys Arg Gly Pro Gln Glu Glu Pro Gly Arg His Lys Ala
340 345 350

Ser Pro Cys Lys Gly Arg Arg Glx Gln Glx Cys Glx Gly Pro Arg Gly
 355 360 365
 Thr Ala Arg Gly Gln Trp Gly Ala Gly Gln Pro Glu Asp Glu Glu Asp
 370 375 380
 Asp Ala Glu Tyr Phe Arg Gln Ala Val Gly Glu Glu Pro Asp Glu Asp
 385 390 395 400
 Leu Phe Pro Thr Ala Ala Lys Arg Arg Arg Gln Gly Gly Leu Leu Ala
 405 410 415
 Lys Lys Gln Arg Gly Phe Glu Gln Arg Pro Gly Asn Lys
 420 425

<210> 17
 <211> 460
 <212> PRT
 <213> Drosophila

<400> 17

Met Gly Gly Lys Lys Val His Pro Lys Thr Arg Thr Ala Ala Phe
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 Lys Ala Ser Glu Pro Ser Glu Ile Val Glu Ala Pro His Ser Phe Val
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 Ile His Arg Gly Leu Ala Cys Pro Tyr Ile Thr Asp Leu Thr Leu Asp
 35 40 45
 Phe Arg Arg Ile Met Glu Pro Phe Thr Ala Ser Asn Leu Arg Glu Lys
 50 55 60
 Arg Met Asn Arg Ile Gln Asp Phe Val Cys Leu Ser Ser Phe Phe His
 65 70 75 80
 Val Ser His Met Gly Ile Phe Asn Lys Ala Ser Ile Gln Leu Ser Phe
 85 90 95
 Lys Val Val Arg Leu Pro Arg Gly Pro Ser Leu Thr Phe Lys Val His
 100 105 110
 Gln Phe Thr Leu Ala Arg Asp Val Ile Ser Leu Ser Lys Lys Gln Met
 115 120 125
 Ile Asp Asn Asp His Phe Lys His Ala Pro Leu Val Ile Met Asn Asn
 130 135 140
 Phe Ser Gly Asp Gly Lys His Leu Lys Leu Met Ala Thr Thr Phe Gln
 145 150 155 160
 Asn Met Phe Pro Ser Ile Asn Leu Ala Thr Val Asn Ile Gly Thr Ile
 165 170 175
 Arg Arg Cys Val Leu Phe Ser Tyr Asn Pro Asp Thr Lys Leu Val Glu
 180 185 190
 Met Arg His Tyr Ser Val Gln Val Val Pro Val Gly Leu Lys Arg Ala
 195 200 205
 Val Gln Lys Ile Val Lys Gly Thr Val Pro Asn Leu Gly Lys Cys Asn
 210 215 220
 Glu Val Val Asp Phe Val Thr Lys Asp Gly Tyr Ala Ser Glu Ser Glu
 225 230 235 240
 Ala Glu Asp Asp Glu Gln Ser His Val Val Leu Ala Gln Thr Leu Lys
 245 250 255
 Ser Lys Gly Asn Leu Glu Asp Lys Lys Ser Ser Ile Lys Leu His Glu
 260 265 270

Ile Gly Pro Arg Leu Thr Met Gln Leu Ile Lys Ile Glu Glu Gly Leu
275 280 285
Leu Thr Gly Glu Val Leu Tyr His Cys His Val Val Lys Thr Glu Asp
290 295 300
Glu Lys Glu Thr Leu Arg Lys Leu Val Glu Lys Lys Arg Lys Gln Lys
305 310 315 320
Glu Gln Arg Lys Lys Glu Gln Ala Glu Asn Arg Ala Phe Asn Leu Lys
325 330 335
Leu Lys Lys Asp Glu Lys Trp Ala Ala Lys Arg Ala Ala Glu Gly Arg
340 345 350
Thr Asp Ser Asp Pro Glu Asp Asp Ala Glu Tyr Tyr Lys Glu Glu Val
355 360 365
Gly Glu Glu Pro Asp Glu Glu Leu Phe Lys Met Glu Ala Lys Ser Ser
370 375 380
Arg Lys Arg Pro Ser Leu Gly Gly Met Lys Tyr Lys Asn Lys Arg
385 390 395 400
Ala Lys Leu Asp Thr Lys Asp Lys Asn Asp Lys Ser Glu Arg Thr Asp
405 410 415
Phe Tyr Asp Arg Lys Cys Lys Phe Asp Arg Lys Asp Lys Lys Asp Lys
420 425 430
Phe Asp Pro Lys Asn Gly Arg Ala Lys Phe Asp Pro Lys Asn Lys Arg
435 440 445
Ala Lys Phe Asp His Pro Lys Ser Arg Lys Ser Lys
450 455 460

<210> 18
<211> 15
<212> DNA
<213> homo sapiens

<400> 18
a~~gg~~ggcgtcgg ggagg

15


<210> 19
<211> 358
<212> PRT
<213> mus musulus

<220>
<221> VARIANT
<222> (1)...(358)
<223> Xaa = Any Amino Acid

<400> 19
Phe Gly Gln Gly Gly Lys Gln Ala Ala Trp Gly Ser Pro Gly Gly Pro
1 5 10 15
Asp Ile Arg Ser Ala Ile Ala Pro Gly Glu Leu Arg Asn Leu Glu Ser
20 25 30
Tyr Ala Ala Gln Pro His Ser Phe Val Phe Thr Arg Gly Arg Ala Gly
35 40 45

Arg Asn Val Arg Gln Leu Ser Leu Asp Val Arg Arg Val Met Glu Pro
50 55 60
Leu Thr Ala Thr Arg Leu Gln Val Arg Lys Lys Asn Ser Leu Lys Asp
65 70 75 80
Cys Val Ala Val Ala Gly Pro Leu Gly Val Thr His Phe Leu Ile Leu
85 90 95
Thr Lys Thr Asp Asn Ser Val Tyr Leu Lys Leu Met Arg Leu Pro Gly
100 105 110
Gly Pro Thr Leu Thr Phe Gln Ile Ser Lys Tyr Thr Leu Ile Arg Asp
115 120 125
Val Val Ser Ser Leu Arg Arg His Arg Met His Glu Gln Gln Phe Asn
130 135 140
His Pro Pro Leu Leu Val Leu Asn Ser Phe Gly Pro Gln Gly Met His
145 150 155 160
Ile Lys Leu Met Ala Thr Met Phe Gln Asn Leu Phe Pro Ser Ile Asn
165 170 175
Val His Thr Val Asn Leu Asn Thr Ile Lys Arg Cys Leu Leu Ile Asn
180 185 190
Tyr Asn Pro Asp Ser Gln Glu Leu Asp Phe Arg His Tyr Ser Val Lys
195 200 205
Val Val Pro Val Gly Ala Ser Arg Gly Met Lys Lys Leu Leu Gln Glu
210 215 220
Lys Phe Pro Asn Met Ser Arg Leu Gln Asp Ile Ser Glu Leu Leu Ala
225 230 235 240
Thr Gly Val Gly Leu Ser Asp Ser Glu Val Glu Pro Asp Gly Glu His
245 250 255
Asn Thr Thr Glu Leu Pro Gln Ala Val Ala Gly Arg Gly Asn Met Gln
260 265 270
Ala Gln Gln Ser Ala Val Arg Leu Thr Glu Ile Gly Pro Arg Met Thr
275 280 285
Leu Gln Leu Ile Lys Ile Gln Glu Gly Val Gly Asn Gly Asn Val Leu
290 295 300
Phe His Ser Phe Val His Lys Thr Glu Glu Leu Gln Ala Ile Leu
305 310 315 320
Ala Ala Lys Glu Glu Lys Leu Arg Leu Lys Ala Gln Arg Gln Asn Gln
325 330 335
Gln Ala Glu Asn Leu Gln Arg Xaa Arg Ser Cys Arg Xaa Pro Thr Arg
340 345 350
Arg Arg Ala Trp Gln Ala
355

<210> 20
<211> 137
<212> PRT
<213> homo sapiens

<220>
<221> VARIANT
<222> (1) ... (137)
<223> Xaa = Any Amino Acid

<400> 20

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Asn Val Tyr Phe Lys Leu Met Arg Leu Pro Gly Gly Pro Thr Leu Thr
20 25 30
Phe Gly Val Lys Lys Tyr Ser Leu Val Arg Asp Val Val Ser Ser Leu
35 40 45
Arg Arg His Arg Met His Glu Gln Gln Phe Ala His Pro Pro Leu Leu
50 55 60
Val Leu Asn Ser Phe Gly Pro His Gly Met His Val Lys Leu Met Ala
65 70 75 80
Thr Met Phe Gln Asn Leu Phe Pro Ser Ile Asn Val His Lys Val Asn
85 90 95
Leu Asn Thr Ile Lys Arg Cys Ser Ser Xaa Asp Leu Lys Pro Gly Phe
100 105 110
Pro Arg Ser Leu Asp Phe Arg Pro Ile Ile Ala Phe Lys Gly Gly Ser
115 120 125
Cys Trp Ala Pro Asn Ser Gly Gly Leu
130 135

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SER. 101



- 1 -

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SEQUENCE LISTING

<110> Welch, Peter J.
Barber, Jack R.

<120> Tumor Suppressor Molecules and Methods
of Use

<130> P-IU 3446

<140> US 09/438,917

<141> 1999-11-12

<160> 20

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 16

<212> RNA

<213> Artificial Sequence

<220>

<223> hairpin ribozyme

<400> 1

acctcccccag aaccctt

"u" instead of "T"

16

<210> 2

<211> 16

<212> RNA

<213> homo sapiens

<220>

<221> misc_feature

<222> (1)...(16)

<223> n = A,T,C or G

"u"

<400> 2

agggnngtccgg ggaggtt

"u"

16

<210> 3

<211> 16

<212> RNA

<213> Artificial Sequence

<220>

<223> hairpin ribozyme

<400> 3

agagtgttaag aaactta

"u"

16

<210> 4
<211> 16
<212> RNA
<213> homo sapiens

<220>
<221> misc_feature
<222> (1)...(16)
<223> n = A,T,C or G

<400> 4
tagtngtcta cactct

<210> 5
<211> 1664
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (103)...(1525)

<400> 5
gcctgatgtc gtcccacgcc gtgccggctc tcagggcgccg gaagttagct ggcacggcc 60
ggaaggcgccg gacgcaggag gcctcggtggaa ggacacagca gc atg gga cag tca 114
Met Gly Gln Ser
1

ggg agg tcc cgg cac cag aag cgc gcc ccg ccc cag gcg cag ctc cgc 162
Gly Arg Ser Arg His Gln Lys Arg Ala Pro Pro Gln Ala Gln Leu Arg
5 10 15 20

—
aac ctc gag gcc tat gcc gcg aac ccg cac tcg ttc gtg ttc acg cga 210
Asn Leu Glu Ala Tyr Ala Ala Asn Pro His Ser Phe Val Phe Thr Arg
25 30 35

—
ggc tgc acg ggt cgc aac atc ccg cag ctc agc ctg gac gtg cgg cgg 258
Gly Cys Thr Gly Arg Asn Ile Arg Gln Leu Ser Leu Asp Val Arg Arg
40 45 50

—
gtc atg gag ccc gtc act gcc agc cgt ctg cag gtt cgt aag aag aac 306
Val Met Glu Pro Val Thr Ala Ser Arg Leu Gln Val Arg Lys Lys Asn
55 60 65

—
tcg ctg aag gac tgc gtg gca gtc gct ggg ccc ctc ggg gtc aca cac 354
Ser Leu Lys Asp Cys Val Ala Val Ala Gly Pro Leu Gly Val Thr His
70 75 80

—
ttt ctg atc cta gca aaa caa gag acc aat gtc tac ttt aag ctg atg 402
Phe Leu Ile Leu Ala Lys Gln Glu Thr Asn Val Tyr Phe Lys Leu Met
85 90 95 100

cgc ctc cca gga ggc ccc acc ttg acc ttc cag gtc aag aag tac tcg Arg Leu Pro Gly Gly Pro Thr Leu Thr Phe Gln Val Lys Lys Tyr Ser	105	110	115	450	
ctg gtg cgt gat gtg gtc tcc tca ctg cgc cgg cac cgc atg cac gag Leu Val Arg Asp Val Val Ser Ser Leu Arg Arg His Arg Met His Glu	120	125	130	498	
cag cag ttt gcc cac cca ccc ctc ctg gta ctc aac agc ttt ggc ccc Gln Gln Phe Ala His Pro Pro Leu Leu Val Leu Asn Ser Phe Gly Pro	135	140	145	546	
cat ggt atg cat gtg aag ctc atg gcc acc atg ttc cag aac ctg ttc His Gly Met His Val Lys Leu Met Ala Thr Met Phe Gln Asn Leu Phe	150	155	160	594	
ccc tcc atc aac gtg cac aag gtg aac ctg aac acc atc aag cgc tgc Pro Ser Ile Asn Val His Lys Val Asn Leu Asn Thr Ile Lys Arg Cys	165	170	175	180	642
ctc ctc atc gac tac aac ccc gac tcc cag gag ctg gac ttc cgc cac Leu Leu Ile Asp Tyr Asn Pro Asp Ser Gln Glu Leu Asp Phe Arg His	185	190	195	690	
tat agc atc aaa gtt gtt cct gtg ggc gcg agt cgc ggg atg aag aag Tyr Ser Ile Lys Val Val Pro Val Gly Ala Ser Arg Gly Met Lys Lys	200	205	210	738	
ctg ctc cag gag aag ttc ccc aac atg agc cgc ctg cag gac atc agc Leu Leu Gln Glu Lys Phe Pro Asn Met Ser Arg Leu Gln Asp Ile Ser	215	220	225	786	
gag ctg ctg gcc acg ggc geg ggg ctg tcg gag agc gag gca gag cct Glu Leu Leu Ala Thr Gly Ala Gly Leu Ser Glu Ser Glu Ala Glu Pro	230	235	240	834	
gac ggc gac cac aac atc aca gag ctg cct cag gct gtc gct ggc cgt Asp Gly Asp His Asn Ile Thr Glu Leu Pro Gln Ala Val Ala Gly Arg	245	250	255	260	882
ggc aac atg cgg gcc cag cag agt gca gtg cgg ctc acc gag atc ggc Gly Asn Met Arg Ala Gln Gln Ser Ala Val Arg Leu Thr Glu Ile Gly	265	270	275	930	
ccg cgg atg aca ctg cag ctc atc aag gtc cag gag ggc gtc ggg gag Pro Arg Met Thr Leu Gln Leu Ile Lys Val Gln Glu Gly Val Gly Glu	280	285	290	978	
ggc aaa gtg atg ttc cac agt ttt gtg agc aag acg gag gag gag ctg Gly Lys Val Met Phe His Ser Phe Val Ser Lys Thr Glu Glu Glu Leu	295	300	305	1026	
cag gcc atc ctg gaa gcc aag gag aag aag ctg cgg ctg aag gct cag				1074	

Gln Ala Ile Leu Glu Ala Lys Glu Lys Lys Leu Arg Leu Lys Ala Gln
310 315 320

agg cag gcc cag cag gcc cag aat gtg cag cgc aag cag gag cag cgg Arg Gln Ala Gln Gln Asn Val Gln Arg Lys Gln Glu Gln Arg
325 330 335 340

1122

gag gcc cac aga aag aag agc ctg gag ggc atg aag aag gca cgg gtc Glu Ala His Arg Lys Lys Ser Leu Glu Gly Met Lys Lys Ala Arg Val
345 350 355

1170

ggg ggt agt gat gaa gag gcc tct ggg atc cct tca agg acg gcg agc Gly Gly Ser Asp Glu Glu Ala Ser Gly Ile Pro Ser Arg Thr Ala Ser
360 365 370

1218

ctg gag ttg ggt gag gac gat cat gaa cag gaa gat gat gac atc gag Leu Glu Leu Gly Glu Asp Asp His Glu Gln Glu Asp Asp Asp Ile Glu
375 380 385

1266

tat ttc tgc cag gcg gtg ggc gag gcg ccc agt gag gac ctg ttc ccc Tyr Phe Cys Gln Ala Val Gly Glu Ala Pro Ser Glu Asp Leu Phe Pro
390 395 400

1314

gag gcc aag cag aaa cgg ctt gcc aag tct cca ggg cgg aag cgg aag Glu Ala Lys Gln Lys Arg Leu Ala Lys Ser Pro Gly Arg Lys Arg Lys
405 410 415 420

1362

cgg tgg gaa atg gat cga ggc agg ggt cgc ctt tgt gac cag aag ttt Arg Trp Glu Met Asp Arg Gly Arg Gly Arg Leu Cys Asp Gln Lys Phe
425 430 435

1410

ccc aag aca aag gac aag tcc cag gga gcc cag gcc agg cgg ggg ccc Pro Lys Thr Lys Asp Lys Ser Gln Gly Ala Gln Ala Arg Arg Gly Pro
440 445 450

1458

aga ggg gct tcc cgg gat ggt ggg cga ggc cgg ggc cga ggc cgc cca Arg Gly Ala Ser Arg Asp Gly Gly Arg Gly Arg Gly Arg Pro
455 460 465

1506

ggg aag aga gtg gcc tga g cccaaagccgc accggagcag cggctggatt Gly Lys Arg Val Ala *

470

1555

gaacgccccca gattggggcc cgagatgtgg ccctcggttt cctttcataa aggagtttg tccccagccc ttccactcca gtaaagaact gaattggcaa aaaaaaaaaa
1615
1664

<210> 6

<211> 473

<212> PRT

<213> homo sapiens

<400> 6

Met Gly Gln Ser Gly Arg Ser Arg His Gln Lys Arg Ala Pro Pro Gln

1	5	10	15												
Ala	Gln	Leu	Arg	Asn	Leu	Glu	Ala	Tyr	Ala	Ala	Asn	Pro	His	Ser	Phe
20	25	30													
Val	Phe	Thr	Arg	Gly	Cys	Thr	Gly	Arg	Asn	Ile	Arg	Gln	Leu	Ser	Leu
35	40	45													
Asp	Val	Arg	Arg	Val	-Met	Glu	Pro	Val	Thr	Ala	Ser	Arg	Leu	Gln	Val
50	55	60													
Arg	Lys	Lys	Asn	Ser	Leu	Lys	Asp	Cys	Val	Ala	Val	Ala	Gly	Pro	Leu
65	70	75	80												
Gly	Val	Thr	His	Phe	Leu	Ile	Leu	Ala	Lys	Gln	Glu	Thr	Asn	Val	Tyr
85	90	95													
Phe	Lys	Leu	Met	Arg	Leu	Pro	Gly	Gly	Pro	Thr	Leu	Thr	Phe	Gln	Val
100	105	110													
Lys	Lys	Tyr	Ser	Leu	Val	Arg	Asp	Val	Val	Ser	Ser	Leu	Arg	Arg	His
115	120	125													
Arg	Met	His	Glu	Gln	Gln	Phe	Ala	His	Pro	Pro	Leu	Leu	Val	Leu	Asn
130	135	140													
Ser	Phe	Gly	Pro	His	Gly	Met	His	Val	Lys	Leu	Met	Ala	Thr	Met	Phe
145	150	155	160												
Gln	Asn	Leu	Phe	Pro	Ser	Ile	Asn	Val	His	Lys	Val	Asn	Leu	Asn	Thr
165	170	175													
Ile	Lys	Arg	Cys	Leu	Leu	Ile	Asp	Tyr	Asn	Pro	Asp	Ser	Gln	Glu	Leu
180	185	190													
Asp	Phe	Arg	His	Tyr	Ser	Ile	Lys	Val	Val	Pro	Val	Gly	Ala	Ser	Arg
195	200	205													
Gly	Met	Lys	Lys	Leu	Leu	Gln	Glu	Lys	Phe	Pro	Asn	Met	Ser	Arg	Leu
210	215	220													
Gln	Asp	Ile	Ser	Glu	Leu	Leu	Ala	Thr	Gly	Ala	Gly	Leu	Ser	Glu	Ser
225	230	235	240												
Glu	Ala	Glu	Pro	Asp	Gly	Asp	His	Asn	Ile	Thr	Glu	Leu	Pro	Gln	Ala
245	250	255													
Val	Ala	Gly	Arg	Gly	Asn	Met	Arg	Ala	Gln	Gln	Ser	Ala	Val	Arg	Leu
260	265	270													
Thr	Glu	Ile	Gly	Pro	Arg	Met	Thr	Leu	Gln	Leu	Ile	Lys	Val	Gln	Glu
275	280	285													
Gly	Val	Gly	Glu	Gly	Lys	Val	Met	Phe	His	Ser	Phe	Val	Ser	Lys	Thr
290	295	300													
Glu	Glu	Glu	Leu	Gln	Ala	Ile	Leu	Glu	Ala	Lys	Glu	Lys	Lys	Leu	Arg
305	310	315	320												
Leu	Lys	Ala	Gln	Arg	Gln	Ala	Gln	Gln	Ala	Gln	Asn	Val	Gln	Arg	Lys
325	330	335													
Gln	Glu	Gln	Arg	Glu	Ala	His	Arg	Lys	Ser	Leu	Glu	Gly	Met	Lys	
340	345	350													
Lys	Ala	Arg	Val	Gly	Gly	Ser	Asp	Glu	Glu	Ala	Ser	Gly	Ile	Pro	Ser
355	360	Asp	365												
Arg	Thr	Ala	Ser	Leu	Glu	Leu	Gly	Glu	Asp	Asp	His	Glu	Gln	Glu	Asp
370	375	380													
Asp	Asp	Ile	Glu	Tyr	Phe	Cys	Gln	Ala	Val	Gly	Glu	Ala	Pro	Ser	Glu
385	390	395	400												
Asp	Leu	Phe	Pro	Glu	Ala	Lys	Gln	Lys	Arg	Leu	Ala	Lys	Ser	Pro	Gly
405	410	415													
Arg	Lys	Arg	Lys	Arg	Trp	Glu	Met	Asp	Arg	Gly	Arg	Gly	Arg	Leu	Cys
420	425	430													

Asp Gln Lys Phe Pro Lys Thr Lys Asp Lys Ser Gln Gly Ala Gln Ala
435 440 445
Arg Arg Gly Pro Arg Gly Ala Ser Arg Asp Gly Gly Arg Gly Arg Gly
450 455 460
Arg Gly Arg Pro Gly Lys Arg Val Ala
465 470

<210> 7

<211> 87

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotides

<221> misc_feature

<222> (1)...(87)

<223> n = A,T,C or G

<400> 7

cgcgtaccag gtaatatacc acggaccgaa gtccgtgtgt ttctctggtn nnnttctnnn
nnnnnggatc ctgttccgc ccggttt

60

87

<210> 8

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 8

gtccgtggta tattacctgg ta

22

<210> 9

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 9

cgaaaccggg cgaaaaacagg

20

<210> 10

<211> 52

<212> RNA

<213> Artificial Sequence

<220>

<223> hairpin ribozyme

<221> misc_feature
<222> (1)...(52)
<223> n = A,T,C or G *m*

<400> 10
nnnnnnnnmag aannnnacca gagaaacaca cguuguggua uauuaccugg ua

52

<210> 11
<211> 27
<212> DNA
<213> homo sapien^S

<400> 11
ccatcctaat acgactcact atagggc

27

<210> 12
<211> 43
<212> DNA
<213> homo sapien^S

<220>
<221> misc_feature
<222> (1)...(42)
<223> n = A,T,C or G

<400> 12
cgatgctcct ctagactcga gggttaccacc tccccgacnc cct

43

<210> 13
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 13
ggccacgcgt cgactagtagtac tttttttttt tttttttv

38

<210> 14
<211> 20
<212> DNA
<213> homo sapien^S

<400> 14
cggttcacccg agatcgcccc

20

<210> 15
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> primer

<400> 15

ggccacgcgt cgactagtagtac t

21

<210> 16

<211> 429

<212> PRT

<213> mus musculus

<400> 16

Met Gly Gln Ser Gly Arg Ser Arg His Gln Lys Arg Asn Arg Ala Gln
1 5 10 15
Ala Gln Leu Arg Asn Leu Glu Ser Tyr Ala Ala Gln Pro His Ser Phe
20 25 30
Val Phe Thr Arg Gly Arg Ala Gly Arg Asn Val Arg Gln Leu Ser Leu
35 40 45
Asp Val Arg Arg Val Met Glu Pro Leu Thr Ala Thr Arg Leu Gln Val
50 55 60
Arg Lys Lys Asn Ser Leu Lys Asp Cys Val Ala Val Ala Gly Pro Leu
65 70 75 80
Gly Val Thr His Phe Leu Ile Leu Thr Lys Thr Cys Asn Ser Val Tyr
85 90 95
Leu Lys Leu Met Arg Leu Pro Gly Gly Pro Thr Leu Thr Phe Gln Ile
100 105 110
Ser Lys Tyr Thr Leu Ile Arg Asp Val Val Ser Ser Leu Arg Arg His
115 Phe 120 125
Arg Met His Glu Gln Gln Pro Asn His Pro Pro Leu Leu Val Leu Asn
130 135 140
Ser Phe Gly Pro Gln Ala Met His Ile Lys Leu Met Ala Thr Met Phe
145 150 155 160
Gln Asn Leu Phe Pro Ser Ile Asn Val His Thr Val Asn Leu Asn Thr
165 170 175
Ile Lys Arg Cys Leu Leu Ile Asn Tyr Asn Pro Asp Ser Cys Glu Leu
180 185 190
Asp Phe Arg His Tyr Ser Val Lys Val Val Pro Val Gly Ala Ser Arg
195 200 205
Gly Met Lys Lys Leu Leu Gln Glu Lys Phe Pro Asn Met Ser Arg Leu
210 215 220
Gln Asp Ile Ser Glu Leu Leu Ala Thr Gln Val Gly Leu Ser Asp Ser
225 230 235 240
Glu Val Glu Pro Asp Gln Glu His Asn Ile Thr Glu Leu Pro Gln Ala
245 Phe 250 Thr 255
Val Ala Gly Arg Gly Asn Met Gln Ala Gln Gln Ser Ala Val Arg Leu
260 265 270
Thr Glu Ile Gly Pro Arg Met Thr Leu Gln Leu Ile Lys Ile Gln Glu
275 Asn 280 285
Gly Val Gly Glu Gly Asn Val Leu Phe His Ser Phe Val His Lys Thr
290 295 300
Glu Glu Glu Leu Gln Ala Ile Leu Ala Ala Lys Glu Glu Lys Leu Arg
305 310 315 320
Leu Lys Ala Gln Arg Gln Asn Gln Gln Ala Glu Asn Leu Gln Phe Ser
325 330 335

Arg Ser Cys Arg Gly Pro Gln Glu Glu Glu Pro Gly Arg His Lys Ala
340 345 350
Ser Pro Cys Lys Gly Arg Arg Glx Gln Glx Cys Glx Gly Pro Arg Gly
355 360 365
Thr Ala Arg Gly Gln Trp Gly Ala Gly Gln Pro Glu Asp Glu Asp
370 375 380
Asp Ala Glu Tyr Phe Arg Gln Ala Val Gly Glu Glu Pro Asp Glu Asp
385 390 395 400
Leu Phe Pro Thr Ala Ala Lys Arg Arg Gln Gly Gly Leu Leu Ala
405 410 415
Lys Lys Gln Arg Gly Phe Glu Gln Arg Pro Gly Asn Lys
420 425

<210> 17
<211> 460
<212> PRT
<213> Drosophila

<400> 17
Met Gly Gly Lys Lys Val His Pro Lys Thr Arg Thr Ala Ala Phe
1 5 10 15
Lys Ala Ser Glu Pro Ser Glu Ile Val Glu Ala Pro His Ser Phe Val
20 25 30
Ile His Arg Gly Leu Ala Cys Pro Tyr Ile Thr Asp Leu Thr Leu Asp
35 40 45
Phe Arg Arg Ile Met Glu Pro Phe Thr Ala Ser Asn Leu Arg Glu Lys
50 55 60
Arg Met Asn Arg Ile Gln Asp Phe Val Cys Leu Ser Ser Phe Phe His
65 70 75 Ile 80
Val Ser His Met Gly Ile Phe Asn Lys Ala Ser Thr Gln Leu Ser Phe
85 90 95
Lys Val Val Arg Leu Pro Arg Gly Pro Ser Leu Thr Phe Lys Val His
100 105 110
Gln Phe Thr Leu Ala Arg Asp Val Ile Ser Leu Ser Lys Lys Gln Met
115 120 125
Ile Asp Asn Asp His Phe Lys His Ala Pro Leu Val Ile Met Asn Asn
130 135 140
Phe Ser Gly Asp Gly Lys His Leu Lys Leu Met Ala Thr Thr Phe Gln
145 150 155 160
Asn Met Phe Pro Ser Ile Asn Leu Ala Thr Val Asn Ile Gly Thr Ile
165 170 175
Arg Arg Cys Val Leu Phe Ser Tyr Asn Pro Asp Thr Lys Leu Val Glu
Arg 180 185 190
Met Pro His Tyr Ser Val Gln Val Val Pro Val Gly Leu Lys Arg Ala
195 200 205
Val Gln Lys Ile Val Lys Gly Thr Val Pro Asn Leu Gly Lys Cys Asn
210 215 220
Glu Val Val Asp Phe Val Thr Lys Asp Gly Tyr Ala Ser Glu Ser Glu
225 230 235 240
Ala Glu Asp Asp Glu Gln Ser His Val Val Leu Ala Gln Thr Leu Lys
245 250 255
Ser Lys Gly Asn Leu Glu Asp Lys Lys Ser Ser Ile Lys Leu His Glu
260 265 270

Ile Gly Pro Arg Leu Thr Met Gln Leu Ile Lys Ile Glu Glu Gly Leu
275 Leu 280 Cys 285
Leu Thr Gly Glu Val Ile Tyr His Asp His Val Val Lys Thr Glu Asp
290 295 300
Glu Lys Glu Thr Leu Arg Lys Leu Val Glu Lys Lys Arg Lys Gln Lys
305 310 315 Phe 320
Glu Gln Arg Lys Lys Glu Gln Ala Glu Asn Arg Ala Arg Asn Leu Lys
325 330 335
Leu Lys Lys Asp Glu Lys Trp Ala Ala Lys Arg Ala Ala Glu Gly Arg
340 345 350
Thr Asp Ser Asp Pro Glu Asp Asp Ala Glu Tyr Tyr Lys Glu Glu Val
355 360 365
Gly Glu Glu Pro Asp Glu Glu Leu Phe Lys Met Glu Ala Lys Ser Ser
370 375 380
Arg Lys Arg Pro Ser Leu Gly Gly Met Lys Tyr Lys Asn Lys Arg
385 390 395 400
Ala Lys Leu Asp Thr Lys Asp Lys Asn Asp Lys Ser Glu Arg Thr Asp
Phe 405 Cys 410 415
Lys Tyr Asp Arg Lys Asp Lys Phe Asp Arg Lys Asp Lys Lys Asp Lys
420 425 430
Phe Asp Pro Lys Asn Gly Arg Ala Lys Phe Asp Pro Lys Asn Lys Arg
435 Phe 440 445
Ala Lys Phe Asp His Arg Lys Ser Arg Lys Ser Lys
450 455 460

<210> 18

<211> 15

<212> DNA S

<213> homo sapien

<400> 18

aggcgctcgg ggagg

15

<210> 19

<211> 358

<212> PRT

<213> mus musulus

<220>

<221> VARIANT

<222> (1)...(358)

<223> Xaa = Any Amino Acid

<400> 19

Phe Gly Gln Gly Gly Lys Gln Ala Ala Trp Gly Ser Pro Gly Gly Pro
1 5 10 15
Asp Ile Arg Ser Ala Ile Ala Pro Gly Glu Leu Arg Asn Leu Glu Ser
20 25 30
Tyr Ala Ala Gln Pro His Ser Phe Val Phe Thr Arg Gly Arg Ala Gly
35 40 45
Arg Asn Val Arg Gln Leu Ser Leu Asp Val Arg Arg Val Met Glu Pro
50 55 60
Leu Thr Ala Thr Arg Leu Gln Val Arg Lys Lys Asn Ser Leu Lys Asp

65	70	75	80
Cys Val Ala Val Ala Gly Pro Leu Gly Val Thr His Phe Leu Ile Leu			
85	90	95	
Thr Lys Thr Asp Asn Ser Val Tyr Leu Lys Leu Met Arg Leu Pro Gly			
100	105	110	
Gly Pro Thr Leu Thr Phe Gln Ile Ser Lys Tyr Thr Leu Ile Arg Asp			
115	120	125	
Val Val Ser Ser Leu Arg Arg His Arg Met His Glu Gln Gln Phe Asn			
130	135	140	His
His Pro Pro Leu Leu Val Leu Asn Ser Phe Gly Pro Gln Gly Met Lys			
145	150	155	160
Ile Lys Leu Met Ala Thr Met Phe Gln Asn Leu Phe Pro Ser Ile Asn			
165	170	175	
Val His Thr Val Asn Leu Asn Thr Ile Lys Arg Cys Leu Leu Ile Asn			
180	185	190	
Tyr Asn Pro Asp Ser Gln Glu Leu Asp Phe Arg His Tyr Ser Val Lys			
195	200	205	
Val Val Pro Val Gly Ala Ser Arg Gly Met Lys Lys Leu Leu Gln Glu			
210	215	220	
Lys Phe Pro Asn Met Ser Arg Leu Gln Asp Ile Ser Glu Leu Leu Ala			
225	230	235	240
Thr Gly Val Gly Leu Ser Asp Ser Glu Val Glu Pro Asp Gly Glu His			
245	250	255	
Asn Thr Thr Glu Leu Pro Gln Ala Val Ala Gly Arg Gly Asn Met Gln			
260	265	270	
Ala Gln Gln Ser Ala Val Arg Leu Thr Glu Ile Gly Pro Arg Met Thr			
275	280	285	
Leu Gln Leu Ile Lys Ile Gln Glu Gly Val Gly Asn Gly Asn Val Leu			
290	295	300	
Phe His Ser Phe Val His Lys Thr Glu Glu Leu Gln Ala Ile Leu			
305	310	315	320
Ala Ala Lys Glu Glu Lys Leu Arg Leu Lys Ala Gln Arg Gln Asn Gln			
325	330	335	
Gln Ala Glu Asn Leu Gln Arg Xaa Arg Ser Cys Arg Xaa Pro Thr Arg			
340	345	350	
Arg Arg Ala Trp Gln Ala			
355			

<210> 20
<211> 137
<212> PRT
<213> homo sapiens

<220>
<221> VARIANT
<222> (1)...(137)
<223> Xaa = Any Amino Acid

<400> 20
Leu Gly Pro Arg Val Thr His Phe Leu Ile Leu Ser Lys Thr Glu-Thr
1 5 10 15
Asn Val Tyr Phe Lys Leu Met Arg Leu Pro Gly Gly Pro Thr Leu Thr
20 25 30

Phe Gln Val Lys Lys Tyr Ser Leu Val Arg Asp Val Val Ser Ser Leu
35 40 45
Arg Arg His Arg Met His Glu Gln Gln Phe Ala His Pro Pro Leu Leu
50 55 60
Val Leu Asn Ser Phe Gly Pro His Gly Met His Val Lys Leu Met Ala
65 70 75 80
Thr Met Phe Gln Asn Leu Phe Pro Ser Ile Asn Val His Lys Val Asn
85 90 95
Leu Asn Thr Ile Lys Arg Cys Ser Ser Xaa Asp Leu Lys Pro Gly Phe
100 105 110
Pro Arg Ser Leu Asp Phe Arg Pro Ile Ile Ala Phe Lys Gly Gly Ser
115 120 125
Cys Trp Ala Pro Asn Ser Gly Gly Leu
130 135